WHAT IS CLAIMED IS:

1. A method for destabilizing non-specific duplex formation between a homopolymeric sequence of an oligonucleotide and a non-homopolymeric target nucleic acid, comprising a modification of said homopolymeric sequence of said oligonucleotide, wherein said modification decreases or abrogates hydrogen bonding between said modified homopolymeric sequence of said oligonucleotide and a non-homopolymeric target sequence.

2. The method of claim 1, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

3. The method of claim 2, wherein said universal base is 3-nitropyrrole.

4. The method of one of claims 1-3, wherein said oligonucleotide is a homopolymer comprising at least one nucleotide modification.

5. A method for increasing the proportion of full length cDNA clones in a library, comprising a use of a modified oligo d(T) homopolymer during first strand synthesis, wherein said modified oligo d(T) homopolymer comprises a modification which decreases or abrogates hydrogen bonding between said modified oligo d(T) homopolymer and a non-homopolymeric target sequence, thereby increasing the proportion of full length cDNA clones.

6. The method of claim 5, wherein said modification is at least one universal base incorporated into said oligo d(T) homopolymer.

7. The method of claim 6, wherein said universal base is 3-nitropyrrole.

8. The method of claim 5, wherein said modification is at least one chemically modified nucleoside incorporated into said oligo d(T) homopolymer.

9. The method of claim 5, wherein said modification is at least one base analog incorporated into said oligo d(T) homopolymer.

10. The method of claim 9, wherein said base analog is inosine.

11. The method of claim 5, wherein said modification is at least one mismatch incorporated into said oligo d(T) homopolymer.

12. The method of claim 5, wherein said modification is a phosphate or ribose modification incorporated into said oligo d(T) homopolymer.

13. The method according to one of claims 5 to 12, wherein an enzyme capable of RNA-dependent DNA polymerization is used for said first strand synthesis.

14. The method according to claim 13, wherein said enzyme is a reverse transcriptase selected from the group consisting of avian myoblastoid virus reverse transcriptase, murine moloney leukemia virus reverse transcriptase, and human immuno deficiency virus reverse transcriptase.

15. A kit for the synthesis of cDNA, said kit comprising a modified oligo d(T) homopolymeric primer, wherein said modified

oligonucleotide includes a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

16. A method for reducing mispriming events during DNA synthesis comprising a use of a modified oligonucleotide to prime said DNA synthesis, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby reducing mispriming events, while maintaining a formation of a duplex with a homopolymeric target sequence.

17. The method of claim 16, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

18. The method of claim 17, wherein said universal base is 3-nitropyrrole.

19. The method of claims 16, 17 or 18, wherein said oligonucleotide is a homopolymer.

20. A method for reducing mispriming during 5' RACE comprising a use of a modified oligonucleotide to prime said 5' RACE, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby reducing mispriming events while maintaining a formation of a duplex with a homopolymeric target sequence.

21. The method of claim 20, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

22. The method of claim 20, wherein said universal base is 3-nitropyrrole.

23. The method of claim 22, wherein said modification is at least one chemically modified nucleoside incorporated into said homopolymeric sequence.

24. The method of claim 20, wherein said modification is at least one base analog incorporated into said homopolymeric sequence.

25. The method of claim 24, wherein said base analog is inosine.

26. The method of claim 20, wherein said modification is at least one mismatch incorporated into said homopolymeric sequence.

27. The method of claim 20, wherein said modification is a phosphate or ribose modification incorporated into said homopolymeric sequence.

28. A kit for 5' RACE comprising a modified oligonucleotide primer, comprising a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

29. A method for reducing mispriming during 3' RACE comprising a priming of said 3' RACE with a modified oligonucleotide, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby reducing mispriming events while maintaining a formation of a duplex with a homopolymeric target sequence.

30. The method of claim 29, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

31. A method for generating *bona fide* genetic markers comprising a use of a modified oligonucleotide to prime from a homopolymeric stretch, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

32. The method of claim 31, wherein said modified oligonucleotide primes from an internal A-rich region in an Alu repeat.

33. A method for stabilizing duplex formation between an oligonucleotide comprising a homopolymeric sequence and a target homopolymeric sequence comprising a modification of said homopolymeric sequence of said oligonucleotide, wherein said modification decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby stabilizing duplex formation between said oligonucleotide and said target sequence.

34. A method for reducing mispriming during sequencing comprising a use of a modified oligonucleotide to prime DNA synthesis, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

35. A method to improve the discrimination between a binding of an oligonucleotide homopolymeric sequence to its targeted homopolymeric sequence versus a non-homopolymeric sequence comprising an insertion into said homopolymeric sequence of said oligonucleotide of at

least one modification which decreases or abrogates hydrogen bonding between same and said non-homopolymeric sequence.

36. A method for increasing the proportion of full length cDNA clones in a library, comprising a use of a modified oligonucleotide during second strand synthesis from a 3' end-tailed first strand product, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby increasing the proportion of full length cDNA clones.

WHAT IS CLAIMED IS:

1. A method for destabilizing non-specific duplex formation between a homopolymeric sequence of an oligonucleotide and a non-homopolymeric target nucleic acid, comprising a modification of said homopolymeric sequence of said oligonucleotide, wherein said modification decreases or abrogates hydrogen bonding between said modified homopolymeric sequence of said oligonucleotide and a non-homopolymeric target sequence.

2. The method of claim 1, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

3. The method of claim 2, wherein said universal base is 3-nitropyrrole.

4. The method of one of claims 1-3, wherein said oligonucleotide is a homopolymer comprising at least one nucleotide modification.

5. A method for increasing the proportion of full length cDNA clones in a library, comprising a use of a modified oligo d(T) homopolymer during first strand synthesis, wherein said modified oligo d(T) homopolymer comprises a modification which decreases or abrogates hydrogen bonding between said modified oligo d(T) homopolymer and a non-homopolymeric target sequence, thereby increasing the proportion of full length cDNA clones.

6. The method of claim 5, wherein said modification is at least one universal base incorporated into said oligo d(T) homopolymer.

7. The method of claim 6, wherein said universal base is 3-nitropyrrole.

8. The method of claim 5, wherein said modification is at least one chemically modified nucleoside incorporated into said oligo d(T) homopolymer.

9. The method of claim 5, wherein said modification is at least one base analog incorporated into said oligo d(T) homopolymer.

10. The method of claim 9, wherein said base analog is inosine.

11. The method of claim 5, wherein said modification is at least one mismatch incorporated into said oligo d(T) homopolymer.

12. The method of claim 5, wherein said modification is a phosphate or ribose modification incorporated into said oligo d(T) homopolymer.

13. The method according to one of claims 5 to 12, wherein an enzyme capable of RNA-dependent DNA polymerization is used for said first strand synthesis.

14. The method according to claim 13, wherein said enzyme is a reverse transcriptase selected from the group consisting of avian myoblastoid virus reverse transcriptase, murine moloney leukemia virus reverse transcriptase, and human immuno deficiency virus reverse transcriptase.

15. A kit for the synthesis of cDNA, said kit comprising a modified oligo d(T) homopolymeric primer, wherein said modified

oligonucleotide includes a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

16. A method for reducing mispriming events during DNA synthesis comprising a use of a modified oligonucleotide to prime said DNA synthesis, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby reducing mispriming events, while maintaining a formation of a duplex with a homopolymeric target sequence.

17. The method of claim 16, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

18. The method of claim 17, wherein said universal base is 3-nitropyrrole.

19. The method of claims 16, 17 or 18, wherein said oligonucleotide is a homopolymer.

20. A method for reducing mispriming during 5' RACE comprising a use of a modified oligonucleotide to prime said 5' RACE, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby reducing mispriming events while maintaining a formation of a duplex with a homopolymeric target sequence.

21. The method of claim 20, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

22. The method of claim 20, wherein said universal base is 3-nitropyrrole.

23. The method of claim 22, wherein said modification is at least one chemically modified nucleoside incorporated into said homopolymeric sequence.

24. The method of claim 20, wherein said modification is at least one base analog incorporated into said homopolymeric sequence.

25. The method of claim 24, wherein said base analog is inosine.

26. The method of claim 20, wherein said modification is at least one mismatch incorporated into said homopolymeric sequence.

27. The method of claim 20, wherein said modification is a phosphate or ribose modification incorporated into said homopolymeric sequence.

28. A kit for 5' RACE comprising a modified oligonucleotide primer, comprising a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

29. A method for reducing mispriming during 3' RACE comprising a priming of said 3' RACE with a modified oligonucleotide, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby reducing mispriming events while maintaining a formation of a duplex with a homopolymeric target sequence.

30. The method of claim 29, wherein said modification is at least one universal base incorporated into said homopolymeric sequence.

31. A method for generating *bona fide* genetic markers comprising a use of a modified oligonucleotide to prime from a homopolymeric stretch, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

32. The method of claim 31, wherein said modified oligonucleotide primes from an internal A-rich region in an Alu repeat.

33. A method for stabilizing duplex formation between an oligonucleotide comprising a homopolymeric sequence and a target homopolymeric sequence comprising a modification of said homopolymeric sequence of said oligonucleotide, wherein said modification decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby stabilizing duplex formation between said oligonucleotide and said target sequence.

34. A method for reducing mispriming during sequencing comprising a use of a modified oligonucleotide to prime DNA synthesis, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence.

35. A method to improve the discrimination between a binding of an oligonucleotide homopolymeric sequence to its targeted homopolymeric sequence versus a non-homopolymeric sequence comprising an insertion into said homopolymeric sequence of said oligonucleotide of at

least one modification which decreases or abrogates hydrogen bonding between same and said non-homopolymeric sequence.

36. A method for increasing the proportion of full length cDNA clones in a library, comprising a use of a modified oligonucleotide during second strand synthesis from a 3' end-tailed first strand product, wherein said modified oligonucleotide comprises a homopolymeric sequence having a modification which decreases or abrogates hydrogen bonding between same and a non-homopolymeric target sequence, thereby increasing the proportion of full length cDNA clones.